

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 17, 2001, 21:12:49 ; Search time 73.55 Seconds
(without alignments)
922.684 Million cell updates/sec.

Title: US-09-456-306-2
Perfect score: 285
Sequence: 1 MAHSVAQQLIDTLEAGCVKR.....CGVGAMIDLARSNIRINPTP 579

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_15:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organella:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1713	57.4	580	2	Q9ZBT3 streptomyc
2	855	28.6	574	2	P96591 bacillus su
3	693.5	23.2	600	2	Q91147 streptomyc
4	637	21.3	553	1	O26576 methanobact
5	616.5	20.7	587	1	O918J0 methanococc
6	576	19.3	577	1	O27493 synchocyst
7	567	19.0	621	2	P73913 methanocyst
8	566.5	19.0	599	1	O08353 methanococc
9	549	18.4	585	8	O19929 cyanidium c
10	546	18.3	612	2	O59950 spiliullina p
11	533.5	17.9	583	2	O66739 aquilex aeo
12	536	17.6	548	2	O916T2 salmonella
13	513	17.2	552	1	O28554 archaeoglob
14	508	17.0	613	2	O92567 streptomyc
15	502.5	16.8	584	2	O9WZ18 thermotoga
16	498	16.7	591	2	O9ZF24 streptococ
17	487	16.6	575	1	O28180 archaeoglob
18	486	16.6	587	8	O63181 porphyridiu
19	490.5	16.4	548	2	O9KVV7 vibrio chol

20	490	16.4	583	2	O9PCG0	O9PCG0 xyliella fas
21	486	16.3	562	1	O9UZ10	O9UZ10 pyrococcus
22	482.5	16.2	681	10	O22578	O22578 volvox cart
23	480	16.1	599	10	O05767	O05767 brassica na
24	475.5	15.9	561	2	P97113	P97113 leuconostoc
25	466.5	15.6	617	2	O59816	O59816 streptomyc
26	461.5	15.5	572	1	O9UWY1	O9UWY1 sulfolobus
27	461.5	15.5	681	10	O49210	O49210 volvox cart
28	461	15.4	594	2	O45396	O45396 corynebacte
29	460	15.4	683	10	O49229	O49229 chlamydomon
30	457	15.3	683	10	O22547	O22547 chlamydomon
31	451	15.1	638	10	O41768	O41768 zea mays (m
32	450.5	15.1	666	10	O9ZSU3	O9ZSU3 bassia scop
33	450	15.1	659	10	O42767	O42767 gossypium h
34	447.5	15.0	601	2	O59272	O59272 caulobacter
35	443	14.8	659	10	O42768	O42768 gossypium h
36	442	14.8	638	10	O41769	O41769 zea mays (m
37	438	14.7	648	10	O41717	O41717 xanthium sp
38	437	14.6	648	10	O41716	O41716 xanthium sp
39	435	14.6	665	10	O38795	O38795 amarantus
40	434.5	14.6	561	2	P94783	P94783 citrobacter
41	429	14.4	575	2	O9ZY10	O9ZY10 neisseria m
42	427.5	14.3	573	2	O9KX90	O9KX90 vibrio chol
43	426.5	14.3	563	2	O68497	O68497 clostridium
44	425	14.2	575	2	O9JY11	O9JY11 neisseria m
45	418.5	14.0	524	1	O27639	O27639 methanobact

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	580 AA.
ID	O9ZBT3			
AC	O9ZBT3;			
DT	01-MAY-1999 (TREMBLrel. 10, Created)			
DD	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DE	01-MAY-2000 (TREMBLrel. 13, Last annotation update)			
DE	PRIVATE DEHYDROGENASE.			
GN	SC1A9.19.			
OS	Streptomyces coelicolor.			
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;			
OC	Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.			
OX	NCBI_TaxID=1902;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-A3(2);			
RA	Saunders D.C., Harris D.;			
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-A3(2);			
RA	Dentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;			
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=9700351; PubMed=8843436;			
RA	Redenbach M., Kleser H.M., Denapalte D., Eichner A., Cullum J.,			
RA	Kinashi H., Hopwood D.A.;			
RT	"A set of ordered cosmids and a detailed genetic and physical map for			
RT	the 8 Mb Streptomyces coelicolor A3(2) chromosome."			
RL	Mol. Microbiol. 21:77-96(1996).			
DR	EMBL: AL034446; CAA22389.1; -.			
DR	INTERPRO: IPR000399; -.			
DR	PFAM: PF00205; TPP_enzymes; 1.			
KW	PRIVATE.			
SO	SEQUENCE 580 AA; 62503 MW; E4708ED5A1C8588 CRC64;			

Query Match 57.4%; Score 1713; DB 2; Length 580;
Best Local Similarity 57.5%; Pred. No. 5.6e-109;
Matches 331; Conservative 92; Mismatches 149; Indels 4; Gaps 4;

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OY 6 AEOILDTLEAGCKRIYIGVDSLNPIYDAVRQ-SDIEVWVHVRNEEAAFAAGASLITG 64
DB 7 AEOFDILTRAGVERLYGVGDSLNPIYDAVRHSHGIEVWVHVRNEEAAFAAGASLITG 66
OY 65 ELAVCAAGCGPNTLHJGLYDSHNGAKVLAIAHSIAQSGFFPOTHEPHEIFKECS 124
DB 67 KTLACAGSCGPNTLHJGLYDSHNGAKVLAIAHSIAQSGFFPOTHEPHEIFKECS 126
OY 125 GYCEWNGEGGERILHHAIOSTMGKGVSVVPIGDI AKEDAGDGYTSNSTISSGTPVY 184
DB 127 HSESLISSKOMPRLQRTAIGHAVGGGVSVSLPQDIADDEPAQGAETALVTS-RPTV 185
OY 185 PDPPTAALVAEAINNAKSVTLFCGAGVKNAAQVLEIAEKSPIGHALGKQVITQHN 244
DB 186 RGDDEIDRLVMIIDADKVTLECGSGTGAHAWEFAGKLAPGHALRKEFTLOYDN 245
OY 245 PREVGSGILGAGVADASNEADLLITLGTDPYSDPLFKD-NVAQVINDGHAIGRTVY 303
DB 246 PIVGSGILGAGVADASNEADLLITLGTDPYSDPLFKD-NVAQVINDGHAIGRTVY 305
OY 304 KYPVTDVAATIENTILPHVKEKTRDSFLDRMLKAHERKLSVVEYTHNVEKHVPIHPEY 363
DB 306 DLAVMGDARETLKCLIPRVEKKRRFLDRMLKHAADALEGVKAYTRKVDKHVPIHPEY 365
OY 364 VASILNEADKDAVFTVDGMCNVMHARYTENPEGRDPSFRHGTMANALPHATGAOS 423
DB 366 VALLDEMDADDVFTVDGMCNVMHARYTENPEGRDPSFRHGTMANALPHATGAOS 424
OY 424 VDRNRQVIAACGDLGMLIGELLTVKLHQLPLKAVVFNNSLGWKLMLVEGDEPFT 483
DB 425 TDRNRQVIAACGDLGMLIGELLTVKLHQLPLKAVVFNNSLGWKLMLVEGDEPFT 484
OY 484 DHEEVNFAELIAAAGKSVRTDPKVRQELALAYPSPVLIDYTDPRNALSIPRTIWM 543
DB 485 ANKNPFAAFAEACGAFGRVKEPKDLAGALKAFKHKGPALVDVTPNALSLIPKISA 544
OY 544 EOVGFSKATRTVFGGAGAMIDLARSNIRNIPTP 579
DB 545 DMVTFRLSASKIVLDGCGVGRMLQMARSNIRNIPTP 580

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RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizi A., Galleron N.,
RA Guthrie S.Y., Glaser P., Goffeau A., Golightly E.J., Grand G.,
RA Gutseppel G., Guy B.J., Haga K., Halech J., Harwood C.R., Hanant A.,
RA Hilbert H., Holstappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Kleier-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
RA Kunita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauch C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetlelle D., Portolillo S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Torato V., Uchiyama S., Vandenbol M., Vannier J., Vassatotti A.,
RA Vial A., Wambutt R., Wedler E., Wedler H., Wellzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RT The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis.
RT Nature 390:249-256(1997).
RL [3]
RP SEQUENCE FROM N.A.
RC STRAIN-168:
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB001486; BAA19271.1;
DR EMBL: Z59106; CAB12241.1;
DR HSSP: P37063; IPOX.
DR INTERPRO: IPR000399;
DR PFAM: PF00205; rpp_enzymes; 1.
DR PROSITE: PS00187; TTP_ENZYMES; UNKNOWN_1.
KW Private.
SQ SEQUENCE 574 AA: 63138 MW: F867A1271B7E9710 CXC64;

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Query Match 28.6%; Score 855; DB 2; Length 574;
 Best Local Similarity 34.1%; Pred. No. 2,6e-50;
 Matches 198; Conservative 120; Mismatches 242; Indels 20; Gaps 10;

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OY 1 MAHSAEQ-LIDTLEAGCKRIYIGVDSLNPIYDAVR-QSDIEVWVHVRNEEAAFAAG 57
DB 1 MAHKTGAQMTLELEQMGVGHVYIGPDSINEFELRHERNOLKFIQTRHEVAAALAA 60
OY 58 ASLITGELAVCAAGCGPNTLHJGLYDSHNGAKVLAIAHSIAQSGFFPOTHEPHE 117
DB 61 AEAKLTGKIGVCLISAGPVAHLNGLYPAKADGAVLAIAQVSGEGGRDPDEIKLE 120
OY 118 IIFKESGCGCEWNGEGGERILHHAIOSTMGKGVSVVPIGDI AKEDAGDGYTSNST 176
DB 121 QMEEDVAVNREHSAESLPDLINQAIIRAYSKGAVLSVSDLEAEIKRREPVTSPV 180
OY 177 ISSGTPVFPDPTAALVAEAINNAKSVTLFCGAGVKNAAQVLEIAEKSPIGHALG 236
DB 181 YIEGN-LLEPKKPOLVTCQAYINNNAKPIILAGOGKKAKRELLEFADRAAPIVVTLPA 238
OY 237 KOYIQHENEPEVMSGLLIGVACVDASNEADLLITLGTDPYSDPLFKD-NVAQVINDG 295
DB 239 KGVPKPHHFLNDQIGIKKPAYEEMECDDLIMGTSPFRDITLPDTPALQIDSDPA 298
OY 296 HIGRTTVKYPVTVG---DVAATIENTILPHVKEKTRDSFLDRMLKAHERKLSVVEYTH 351
DB 299 KICKR-----YPIVAGLVOSALGLRELTYEIKEDRRFLINACTEEMQWMEIEKEDFT- 353
OY 352 NVEKHVPIHPEYVIAASLNEADKDAVFTVDGMCNVMHARYTENPEGRDPSFRHGT 411
DB 354 --EATTPKPKQGVVARLOEAAADDAVLSVGVTVTWMAKHFH-MNANQDFIVSSWLAM 410
OY 412 ANMLPHAIAGQSVDRNRQVIAACGDLGMLIGELLTVKLHQLPLKAVVFNNSLGWKL 471

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Db 411 GCGILPGIAASLSEPERQALAVCGDGFSAWMDLPTAVVYKYLPTVILNNENLGIEX 470
Oy 472 EMLVEGPERGTDEEENFAEIAAAGIKSVRTIDPKVREQLAEALAYGPLYIDVTD 531
Db 471 EGVKNCIDIVVTLQNVDAFAEASCACAKIKTKAEELPAFHEALHSDQPVVDMIG 530
Oy 532 PNAISIPPTITWQVGFSAKATRTVEGGVGMATLARS 571
Db 531 -NEPLPGKITTYGAKGFSKYLKNEFENQKFEKPSLAKS 569

RESULT 3
Oy 09L147 PRELIMINARY: PRT: 600 AA.
AC 09L147:
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE PUTATIVE PYRUVATE DEHYDROGENASE (PYRUVATE OXIDASE).
GN SC6D11.08.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxId=1902;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Thompson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.
RN 13
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Redenbach M., Kleiser H.M., Denapalte D., Eichner A., Cullum J.,
RA Klinosh H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL: AL158061; CAB76331.1; -.
KW Pyruvate.
SQ SEQUENCE 600 AA: 65282 MW: A5DDDA8382B7D90F CRC64;
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Db 305 MIGIRYPMDAHLVSDSRETLRALIPMLQRRKKDRGMREKIEK-DVREHMDLCDRR---AGE 360
Oy 356 HV--PIHEEVASLTNLAKDAVFTYDTMGCNVNHARIYIENPGSTDDPFGSFGHGTMAN 413
Db 361 HEGKTTNPQAVVAEELSLARLPDDVLTLTADSGSTWMAHRLH---LRDGMQASLSCTLAT 416
Oy 414 ---ALPAIAQASVDRNRQVYIACGDCGLML-LGELLTVKLH-----QLPKAVFNN 463
Db 417 MGGTPTAIAARFAYPERPIAFTGDGAFQMGNGENMTYKRYIDRLSGSAPLIFCYFNN 476
Oy 464 SSLGMVKLEM-LVEGDEF--GTDHEEVNFAEIAAAGIKSVRTIDPKVREQLAEALAY 520
Db 477 QDLNQVTEORAMAGDKPKYGSODIPDVPYAAVALLGLKGIYCDPDKKGAAMDALSA 536
Oy 521 PGPLYIDVTDNPAISIPPTITWQVGFSAK 553
Db 537 GRPVLEFQVDAETAPIPHMKRQKKAIAA 569

RESULT 4
Oy 026576 PRELIMINARY: PRT: 553 AA.
AC 026576:
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE PYRUVATE DEHYDROGENASE / ACETOLACTATE SYNTHASE.
GN MTH476.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanobacterium.
OX NCBI_TaxId=2166;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN-DELTA H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A.;
RA Aldredge T., Bashirzadeh R., Blakey D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Potlher B., Qiu D.,
RA Spadafora R., Vicare A., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Sifer H., Patveil D., Prabakar S.,
RA McDougall S., Shiner G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Nollan J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics."
RL J. Bacteriol. 179:7135-7155(1997).
DR EMBL: AE000832; AAB84982.1; -.
DR HSSP: P00269; 1RB9.
DR INTERPRO: IPR000399; -.
DR INTERPRO: IPR001052; -.
DR INTERPRO: IPR003252; -.
DR PFAM: PF00205; TTP_enzymes; 2.
DR PFAM: PF00301; rubredoxin; 1.
DR PRODOM: PD001610; -. 1.
KW Pyruvate.
SQ SEQUENCE 553 AA: 60506 MW: 17B385DE4A4EC938 CRC64;
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Query Match 23.2%; Score 693.5; DB 2; Length 600;
Best Local Similarity 31.4%; Pred. No. 3, 1e-39;
Matches 180; Conservative 108; Mismatches 252; Indels 33; Gaps 12;
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Query Match 21.3%; Score 637; DB 1; Length 553;
Best Local Similarity 30.4%; Pred. No. 2e-35;
Matches 164; Conservative 95; Mismatches 224; Indels 56; Gaps 6;
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Db 175 VYNNMLVSPDEAEALREAVKHAILERGVSHYDVPDV-----QTMECTAPVK 222
OY 184 -----VPPDTEAALALVEAINNAKSVTLFCGAGYKNAPOYLEAEIKSPGIA 233
Db 223 PLRGMMAEAAVPPRRRLAAADLINRAERPIYIAGFGALAEADSVLEAERIGAIYST 282
OY 234 LGKQVIOHENEFEVMSGLIGYACVDASNEADLLILGTPEPPYSDLPKNNVAQVDIN 293
Db 283 FRKQGLVNDYDLYLSCGSLGSAALAEVKKADLLVIGSSFDLTRPPRRITLOVDID 342
OY 294 GAHGRRTTVKPYVGDVAATIENTILPHVKEKTRSDRLMLKAHRRKLSVVEITYTHV 353
Db 343 PMMVARRHVEBGLRSSLIVGELISWEKEKRGPIYLAELGELRDEMGLLESEADPSL 402
OY 354 EKHVPIHPEYVASINELADKDAVFTVDTGMCNWKARIENEGEGRDVGSRHGTMAN 413
Db 403 R--PIRPQYIISVLRRELDLDDAIIITLDVGENMWPGRNQ--MKSTRGSPFOYTWGSMGF 458
OY 414 ALPHAIQAQSVDRNRQIVAMCGGGLGMLGELLIVKILHQLPLKAVFNNSSILGMYKLEM 473
Db 459 GLPAAIAQLEFPDRQVCL-----NNRNLAIMIQEO 490
OY 474 LVGEQDEFTDEHEVNAETIAAAGIKSVRIIDPKKVRQOLAALAYPGPVLIDIVTP 532
Db 491 RVGCFVWQTELODCDFAGFAENCGRGLRVDPDGLEDVSREALGTGDPVLVIDETDP 549

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RESULT 5
OY98J0 PRELIMINARY; PRT; 587 AA.
AC 09Y8J0;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ACETOHYDROXYACID SYNTHASE LARGE SUBUNIT (EC 4.1.3.18).
GN ILVB.
OS Methanococcus maripaludis.
OC Archaea: Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=39152;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=JJ;
RA Gardner W.L., Whitman W.B.;
RT "Development of integrative and shuttle vectors for Methanococcus
RL maripaludis";
CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
DR EMBL: AF118061; AAD28737.1; -.
DR HSSP: P06169; LPVD.
DR INTERPRO: IPR000399; -.
DR PFAM: PF00205; TPP_enzymes; 1.
DR PROSITE: PS00187; TPP_ENZYMES; 1.
KW Lyase; Flavo-protein; Thiamine pyrophosphate.
SQ SEQUENCE 587 AA; 63837 MW; A31D942AA71FE440 CRC64;

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Query Match 20.7%; Score 616.5; DB 1; Length 587;
Best Local Similarity 29.9%; Pred. No. 5.5e-34;
Matches 167; Conservative 110; Mismatches 250; Indels 31; Gaps 13;
OY 6 AEOLIDLEAGVKRYIGLVGDSINPIVDVAVROSIDEMVHVRNEAFAAGASLITGE 65
Db 4 AEMAKMLEAENKVLFGYFGGOLLPPYDALYQSDFLHILTRHQAANAHAADGVARASGD 63
OY 66 LAVCAASGFGCNTHLIGLVDSHRNGAKVLAISHIPSAOIGSTFOETHPEILFKECSC 125
Db 64 VGVCAVATSGCATNLVGVATAHADSSPVVALTGVQVPTKLIGNDAPFOEIDALGIFMTK 123
OY 126 YCEVNVNGDEGERTLHAIQSTMAKG--GVSVVYIPGDIAMEDAGDGY---SNSTISSGT 181
Db 124 HNFQIOKTSLEPKIFERRAFIAKTGRGAVAVHVDLPKVDVODDLDEKYPPIPAETINLGCK 183

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OY 182 PVFPDPTPEAALALVEAINNAKSVTLFCGAGYK--NARAQVLEAEIKSPIGHALGKQY 239
Db 184 PTKFPHPIQIKAAALMLKIAQRPVLIAGGVOGLANAFELIKLSEYADIPCTTLMGKV 243
OY 240 IOHENEFEVMSGLIGYACVDASNEADLLILGTDF-----PISDLPKPDNAQVDIN 293
Db 244 FPEEHRPLSIGVMGMGTQASNSVYESDVLIAIGRFSRITRGDLSFAPNTKVIHIDID 303
OY 294 GAHGRRTTVKPYVGDVAATIENTILPHY--KEKTRSDRLMLKAHRRKLSVVEITYTH 351
Db 304 PAELGNVGVDPITVGDAAKAILKILILMKKEKMYNKTENMENVKLOKKSPPWEEF--- 360
OY 352 NVEKHVPIHE--YVASINELADKD-----AVFTVDTGMCNWKARIENEGTRDVGVS 405
Db 361 ---DMPTRPKQKIVIEEMAAALREVPDGLNTVLTITDVGQNNMMAHYPTQ--SAPKSFSS 416
OY 406 FRHGTMANALPHAIQAQSVDRNRQIVAMCGGGLGMLGELLIVKILHQLPLKAVFNNSS 465
Db 417 GGQGTMGEGFPAAIGAKFARPANVIAVGDGFLMNSQELATVIEYELPIVIVTFDKRT 476
OY 466 LGMV--KLEMLVEGQPEFGTD--HEEVNAETIAAAGIKSVRIIDPKKVRQOLAALAYPGP 523
Db 477 LGWVIOWQNLTYGKKQCAVHGLGETPDTIKLAEYIGALRVKRPEDINEAFKTLANSKRP 536
OY 524 VLIDIVTPN-AL-STPP 539
Db 537 YLLDITIDPSEALHMYPP 554

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RESULT 6
OY27493 PRELIMINARY; PRT; 577 AA.
AC 027493;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ACETOACTATE SYNTHASE, LARGE SUBUNIT.
GN MTH144.
OS Methanobacterium thermoautotrophicum.
OC Archaea: Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanobacterium.
OX NCBI_TaxID=2166;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=DELTA H;
RA MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Delonghery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Sater H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pletrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
CC -1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
DR EMBL: AE000905; AAB85919.1; -.
DR HSSP: P06169; LPVD.
DR INTERPRO: IPR000399; -.
DR PFAM: PF00205; TPP_enzymes; 1.
DR PROSITE: PS00187; TPP_ENZYMES; 1.
KW Flavo-protein; Lyase; Thiamine pyrophosphate.
SQ SEQUENCE 577 AA; 62674 MW; A9318489D2D77142 CRC64;

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Query Match 19.3%; Score 576; DB 1; Length 577;
Best Local Similarity 26.8%; Pred. No. 3.1e-31;
Matches 149; Conservative 117; Mismatches 267; Indels 24; Gaps 9;
OY 7 EOLIDTLEAGVKRYIGLVGDSINPIVDVAVROSIDEMVHVRNEAFAAGASLITGEL 66
Db 8 QATIRSLDQADTVFVFGGOLLPLXMDLYDSEILHILVRHQAANAHAADGVARASGRV 67

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OY 67 AACAAAGCGGNNHLLQGLDVSRRNCKAVLAISHIPSAQSGSPFEPOTREHLEIFKECSGY 126
 Db 68 GVCATISGGGATNLVTGITAATMDSPAIYALAGVYTHLIGNAFQFQVDMIGTMTPTKH 127
 OY 127 CEMVNGCEGGERILHHAIIQSTMACK-GVSVVYPCDIAEADAGDGTYSNSTISSGTPPVF 185
 Db 128 SFQPSDASEIPAIYRASFFIAKTGRGCPVVIDLPKIDQCEIME-EVDDLELPGYRPNVK 186
 OY 186 PDPTFAALVLEINNAKSVTLFCGAGV--KNRAQVLELAERIKSPHGLHGGKOYIQHE 243
 Db 187 CHPLDIKRAAELIRSEKPVIIAGGVIIISGASREIKELSDLIKAVVTTTLTGKGSFPED 246
 OY 244 NPFEVGMSSQLCYGACVDAASNEADLLILIGTFP-----YSDFLPKDVAQVINGCAHI 297
 Db 247 HPSANGMIGMIRKVAANLVDECDCLIANGCRSDDTTCNVAFANARIINHVIDDPAEI 306
 OY 298 GHRITVYKPPVYGDAVTAETENILPHVK--EKTDRSFLDRMLKAHERKLSSVETVYTHNVEK 355
 Db 307 GKNVGDVDPVIVDARNVLEKELIAKLYKKRDSQWLESYOKFR-----ADCMPRMSYD 359
 OY 356 HVPFIPEVYASITLNEADDAVEYTDVTCGNWHAHYINPESTRDFVGSFRIGTMANAL 415
 Db 360 EYPLRPQOVIKEITSOVLDEIVYTTDVGONOMMAHFYTS-RAPRKFISSGGLGTGCGFR 418
 OY 416 PHAIGASQVDRNRKQYIAMCGDGLGMLIGELLTVKLIHQPLKAVENNSISAGKCKEMLV 475
 Db 419 PAIATGAKVALPDSVAVAVGCGDGLFLWVCODLATIREYDIPVVICIMDNRIHGLGVAQORL 478
 OY 476 EGQPEFGTDD--EENFALIAAAGIKSVRIYDPKKVRRQDLAEALAPGVGLIDYITDPN 533
 Db 479 FYDERMSTHSLCEVDPFVLAESFVEAERIEEPGTSFALSRAISGEPALDIVIDPD 538
 OY 534 AL-SIPPTITWEQVYG 548
 Db 539 EILPMVPPCGGLTEIVG 555
 RESULT 7
 P73913 PRELIMINARY: PRT: 621 AA.
 AC P73913;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE ACETOHYDROXY ACID SYNTHASE.
 GN ILVG.
 OS *Synechocystis* sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; *Synechocystis*.
 OX NCBI_TaxID=1148;
 RP [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirosewa M., Sugitara M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nariu K., Okumura S.,
 RA Shlump S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tanaka S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT *Synechocystis* sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 DR EMBL: D90910; BAA17977.1; -;
 DR HSSP: P06169; IPVD
 DR INTERPRO: IPR000399; -;
 DR Pfam: Pf00205; TTP_enzymes; 1.
 SO SEQUENCE 621 AA; 67730 MW; 1A1A66C370AE9C34 CRC64;

Query Match	19.0%;	Score 567;	DB 2;	Length 621;
Best Local Similarity	27.4%;	Pred. No. 1.5e-30;		
Matches 164;	Conservative 113;	Mismatches 236;	Indels 86;	Gaps 18

QY	9	LIDTLEAGVYRIGVLVDSINPIYDAVROQ-----SDIEMVYVNRDEEAAFPAGAESILTG	64
Db	27	LMDSLKRGVYKHIGIEYRGGALLPIPYDELYXREMAGEIHHILVNRHOGSHNADGYARTGC	86
QY	65	ELAVCAASCGFGENTHLOGLYDSHNRGAKVLAISHIPSAOIGSTFEOE-----THPEI	110
Db	87	KVGVCFGTSGGATMLVYGINAHNLDSPVYVITGVGVGRAMISGDAFOEIDIFGILPIV	140
QY	119	LFKESGSGCEMVNGEGSERLILHNAIGSTMAKG-GVSVYVYIPGDIKE-----DAGDG	170
Db	147	-----KISUYVRSASDAMKARIVTAEFNLASTGRGQPVILIDIPKDVGESECEYILDPGD-	199
QY	171	TYSNSTISSGTPLYVPRDTEAAALVEALNNKSTYLFECSAG--VKNRAOVLLEAEIKS	222
Db	200	-----VNLPGYPTTKAGNPRQINAAILOLEQARNPLLYGGALANAHAOQEFRAERQOL	255
QY	229	PIGHALGSKOYIOPENPREVEVMSGLLGYGACVDASNEADLLILGTDF-----PYSDFL	287
Db	256	PVTTLTMIGTGFEDENHPLSVGMILGNHGTAYANPAVSECDLLILANGARRDDVGTCKLDEFA	311
QY	283	PKDNVAOVDINGANIIGRTTYKYKRVTDGVAATENILPRYKE-----KTRDSFLDRLM	333
Db	316	SRAKVINDIDIPRAEYGGKNRARDVYIGVGRVHLEQLORAEELDYPTPHNTQAMLNR--	372
QY	336	KAHEKLISSVVEYETHNNEKIVPRINREYVA--SILNELADK--DAVFTVDTGMCNVNHAH	397
Db	374	-----IDHMETDTPLOVPRHVEDIYAEQVYVNEHGRAPARAYTTDVGONOMNAO	423
QY	392	YIENEGTRDFVSGFRHGTMTANALPHALGAOSVDRNROVIAMCGDGGMLIGELTIVKL	451
Db	424	PLNN--GRRRIISAGLSGTMGFGRPAMNGALVGVGDEAVICISDASATOMMLDELGTIAQ	487
QY	452	HQPLKAAVENNSSLGMYK-----LEMLVEGOREFGTDHBEVNFALIAAAGI	495
Db	482	YDIOKTYITLNNNGOAGYRQOQOFEERYEASASNNSGMP-----DINL--LCEAYGI	533
QY	500	KSVRTIDPKKVRBOELAEALVAGVLLDIYV--DPNML-STPRTITVPOVGVCFKATR	555
Db	533	KGIYTRKREDIARPAIEKILANGVAVMDVYVKKDENCYRMLAPRMSNMOYKIGREVPVR	591

RESULT	ID	PRELIMINARY:	PRN:	599 AA:
008353				
AC	008353			
DT	01-JUL-1997 (TREMblrel_04, Created)			
DT	01-JUL-1997 (TREMblrel_04, Last sequence update)			
DT	01-MAY-2000 (TREMblrel_13, Last annotation update)			
DE	ACTOXYDROXYACID SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)			
DE	(ACTOLACTATE SYNTHASE).			
GN	ILVB.			
OS	Methanococcus aeolicus.			
OC	Archaea: Euryarchaeota: Methanococcales; Methanococcaceae;			
OC	Methanococcus.			
OX	NCR1_TaxID=42879;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97254452; Pubmed=9099862;			
RA	Bowen T.L., Union J., Tumbula D.L., Whitman W.B.:			
RT	"Cloning and phylogenetic analysis of the genes encoding			
RL	actoxydroxyacid synthase from the archaeon Methanococcus aeolicus.";			
CC	Gene 188:77-84(1997).			
CC	-1- CATALYTIC ACTIVITY: 2-ACETOLACTATE + CO(2) -> 2 PYRUVATE.			
CC	-1- COFACTOR: THIAMIN PYRROPHOSPHATE.			
CC	-1- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.			
DR	EMBL: U35458; AAB53488.1; -			
DR	INTERPRO: IPR000399; -			
DR	PFAM: PF00205; TPP_enzymes; 1.			
DR	PROSITE: PS00187; TPP_ENZYMES; 1.			
QO	Lyase: Flavoprotein; Thiamine pyrophosphate.			
QO	SEQUENCE 599 AA: 65423 MW: 59630C57DECE062 CRC64;			

DE ENZYMES), SCORE=952.6, E=1.5E-295, N=1.
 GN ILV6.1.
 OS Salmonella typhimurium LT2.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=99287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SSGSC1412;
 RA MashU:
 RT "The Salmonella typhimurium Genome Sequencing Project";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SSGSC1412;
 RA Waterston R.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF233324; AAF3483.1;
 SO SEQUENCE 548 AA; 59224 MW; 6587AAE9E6E2BE04 CRC64;

Query Match 17.6%; Score 526; DB 2; Length 548;
 Best Local Similarity 30.5%; Pred. No. 7.5e-28;
 Matches 168; Conservative 90; Mismatches 240; Indels 52; Gaps 16;

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6 AEGLDLLEAGGVKRTYGVGSLNPIVDVARSQSDIEWVHNEBAFAAGAESLITGE 65
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
4 AOMVYHALRAQGVKTVFGYFGAIPVVDALYDGVENILCHHEGAAAGVARSSTCK 63
66 LAVCAASGCPGNTLHIOGLYDSHRNGAKVLAISHIPSAQIGSTFEQTHPEILKESG 125
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
64 TGVCIATSGPGATNLITGLADLLDSVPVAVITGVSAFETDAFOEDVYGLSLACK 123
126 YCEWNGGEGGRILLHAIQSTMAK-GSVYVVIIGDIAKEAGGCTYSNSTISSGTPV 184
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
124 HSEIVQSLSEELPRIMEAEFVANNAGRPGLVDIPKDI--OLASGELEPWFTVANEAT 180
185 FP--DPTAAALVEAINNASKSVTLFCGAGVKNARA--QVLELAERIKSPIGHALGKOYT 240
181 FPQADVEGARQMLE---QAKRKMLVGVGGVGMAGVAPALRKTIATQMPVCTLGGLAV 237
241 OHENPEVNGSGLLGYGACVDASNEADLLILGTDF-----PYSDFLPKDVAQVDING 294
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
238 EADYVYUIGMIGMGTKANFVQECDLLIAVGARFDDRVTKLTFFANASVIMHMDIP 297
225 AHIGRTTVKVPVDTGVAATENTILPHYKE--KFD--RSFLDRMLKAHERKLSVVEYET 350
228 AEMKRLQAHVALQGD---LNSLLPALQDPLKIDAMROSCAELAEHNAH-----YD 346
351 HNEKHEVPIHEPVASITNELADK--DAVFTVDTCMCNVWHARYT--ENPEGRDFVGS 405
347 H-----PGETIYAPLLLKQLSERKPADSVVTTDVGOMQSAQMHYTRPE---NFITS 397
406 FRHGTMANALPHAIGASVDNRROYIAMCGDGLGMLLGLLTVLKHOLPLKAVVFNNS 465
398 SGLTGMGLPLAAVGAAPNDYVICISGDSFMMNVQELGTVRKQOLPLKIVLLDNR 457
466 LGMVLEMLVEGQPEFG---TDHEEVNPAETIAAAGIKSVRTTPPKKRLQALALAP 521
458 LGMVQMOQLFEQERYSETTLTDND--FLMLASAFIPGCHITRKDDVEALDMLASE 515
522 GPVLIDIVTD 531
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
516 GPYLLHVSID 525

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RESULT 13
 028554 PRELIMINARY; PRT; 552 AA.
 AC 028554;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)

DE ACETOLACTATE SYNTHASE, LARGE SUBUNIT (ILV-1).
 GN AF1720.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
 OC Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Goeyne J.D., Weidman J.F., McDonald L., Uterback T.,
 RA Colton M.D., Spriggs T., Atliach P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 RT reducing archaeon Archaeoglobus fulgidus.";
 RL Nature 390:364-370(1997).
 CC -I- SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
 DR EMBL: AE000985; AAB89531.1; -.
 DR HSSP: P37063; 1POX.
 DR TIGR: AF1720; -.
 DR INTERPRO: IPR000399; -.
 DR PFAM: PF00205; TPP_enzymes; 1.
 DR PROSITE: PS00187; TPP_ENZYMES; 1.
 KW Hypothetical protein; Flavoprotein; Lyase; Thiamine pyrophosphate.
 SO SEQUENCE 552 AA; 59974 MW; 69A4132C525F8245 CRC64;

Query Match 17.2%; Score 513; DB 1; Length 552;
 Best Local Similarity 26.7%; Pred. No. 5.9e-27;
 Matches 153; Conservative 104; Mismatches 259; Indels 56; Gaps 13;

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6 AEGLDLLEAGGVKRTYGVGSLNPIVDVARSQSDIEWVHNEBAFAAGAESLITGE 65
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
4 ADAIKALEMEIEVYFGIPGAIIEVDALYDSGIRHTTTHHEGATHAAGVARSCK 63
66 LAVCAASGCPGNTLHIOGLYDSHRNGAKVLAISHIPSAQIGSTFEQTHPEILKESG 125
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
64 VGVARATSGPGATNVGTGATAYMSSPLVFTGVGPTSMIGNDAFOEDITGITMPTIK 123
126 YCEWNGGEGGRILLHAIQSTMAK-GSVYVVIIGDIAKEAGGCTYSNSTISSG-TPV 183
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
124 HNYLVTDTRKDLGTKEAHHASTGRPGVLVDLKRDTTADI--DFNPKVYSLPGYRK 182
184 VPPDTEAAALVEAINNASKSVTLFCGAGV--KNARQVLELAERIKSPIGHALGKOYT 241
183 LEGRHQLAKAAMELIMKARPYVILAGGVYIISNAKELVELAETIPAFVYITLMKGSIP 242
242 HENPEVNGSGLLGYGACVDASNEADLLILGTDFPYSD-----FLPKDVAQVDIN 293
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
243 EHNPRSLIGFAGMGTIKYANALYESDILLAVGCRF--SDRTTGNAVAMPFAEKIHHID 300
294 GHHIRRTTVKVPVDTGVAATENTILPHYKEKTDSPFLDRMLKAHERKLSVVEYETHNV 353
301 PAETIGKRVDPVIVGDA-----RKVLAKLKAAYEYKORKEWEDKRVNDW 344
354 EKHVP-----HPEYVASITNELADKDAVFTVDTCMCNVWHARYTENPEGRDFVGSF 406
345 KRRPYLKYYKEGFKROYIERACELM-PDAITTEVGQNMMAQFRT-KYRQFLISG 402
407 RHGTMANALPHAIGASVDNRROYIAMCGDGLGMLLGLLTVLKHOLPLKAVVFNNS 466
403 GLGTGFGFPAMGAQVAFPEKTVIDIGDSFPMNIDLATCVYVEIPVVKLVNNGLT 462
467 GNVKLEMLVEGQPEFGTDH-----EEVNPAETIAAAGIKSVRTTPPKKRLQALAL 518
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |

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DB 463 GWR-----OMDELYRENSATCIGCEKTCFEALRGALGCMVTEKSEVDALKEAK 517
 QY 519 AVGPVLIDIVDPNA---LSIPRTTMEQVM 547
 DB 518 EVDAPVVIDPVDYQANVPMFPGALNEII 549

RESULT 14
 ID 092567 PRELIMINARY: PRT: 613 AA.
 AC 092567:
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
 DE ACETOLACTATE SYNTHASE.
 GN SC8D9.24.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxId=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2):
 RA Murphy L., Harris D.;
 RL Submitted (Feb-1999) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2):
 RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (Feb-1999) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2):
 RA MEDLINE=97000351; PubMed=8643436;
 RA Redenbach M., Kleiser H.M., Denapalte D., Eichner A., Cullum J.,
 RA Klashni H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 DR Mol. Microbiol. 21:77-96(1996).
 DR EMBL: AL035569; CAB37588.1;
 DR INTERPRO: IPR000399;
 DR INTERPRO: IPR000847;
 DR PFAM: PF00205; TPP_enzymes; 1.
 DR PROSITE: PS00044; HTL_LYSR_FAMILY; UNKNOWN_1.
 DR PROSITE: PS00187; TPP_ENZYMES; UNKNOWN_1.
 SO SEQUENCE 613 AA; 65223 MW; 8F1378EB37003429 CRC64;

Query Match 17.0%; Score 508; DB 2; Length 613;
 Best Local Similarity 27.3%; Pred. No. 1,5e-26;
 Matches 153; Conservative 105; Mismatches 273; Indels 30; Gaps 11;

QY 6 AEOLIDLEAGVKRYGLVGSLSNPIYDAVROSD-TEVHVHNEEAFAAGAESLITG 64
 DB 28 AOSLRSELEVADVFCIPGCTILPAYDPLMDSTFVRVILVHNEGACAAATGYAQAAG 87
 QY 65 ELAVCAASGPGNTILIGLVDLSHRNGAKVLAISHIPSAOSSTFGFOTHEPILKKES 124
 DB 88 KYGVCAISGPGATNLVPTIADANLDSPLVAITGOVSSALGTDAFQEDVDIGITMPT 147
 QY 125 GYCEVNGEGERILHNAIQTSMACK-GSVVVIIPGDIKAKEDAGDGTYSNSTISSGTPV 183
 DB 148 KISFLVTKAKEDIPRIVQNFHIASTGRPGVPLVDIPKLOKTTFSNRPVMDLPQIRRY 207
 QY 184 VERPDEALALVAINNAKSVTLFCGAGVKMAR--AQVLELAEKIKSPIGHALGKQYQ 241
 DB 208 TRPAAQIIEAAKLLISAARPVLYCGVLAKAKATAEILKVLAEITGAPVTTTLMALGAP 267
 QY 242 HENPREVNGSGLLGACVADSKEADLLLLGTDF-----PSSDLPRDNVAQVINDA 295
 DB 268 DSHPLVIGPGRMGHGAVTATATLQKADLVALGARFDDRVATGKIDSPFAKTIHADIDPA 327
 QY 296 HIGRRTTVVPTGVAAATIENTILPHVKEKTDSPFLDRMLKAHERKLSVETVY--HNW 353

DB 328 EICKNRADVPPIVDAREVADLVQAQVKEKEDGNKCD--YSAMKDLSSRMDTYPLIGDQ 386
 QY 354 EKRVPIHPPEVYASILNELADKDAVFTVDGMCVNHARIENEGRDYFSGRRHGTMAN 413
 DB 387 PEDGSLSPQOQVIERIGOLAPEGTIFPAAGVGOHQMAHFPVQY-EKDPATVNSGCACTMG 445
 QY 414 ALPHAGASVDNRROVIAACGGDGLMGLLGLTYKLLHQLPKAVVFNSSLGMYK-LE 472
 DB 446 AVPAAGAAQAGMPGRTVMALIDGCGFQMTNOELTTALNNIPKAVYINNGALGMVROWO 505
 QY 473 MVEGQPEFGT-----DHEEVN-----FAEIAAAGIKSVRTDPKRYEQALAEAL 518
 DB 506 TLFYNGRYSNTVLHSGPDVNPPEARCTRPVDFVKLSEAMCVCYAIRREDPADLDKVEAN 565
 QY 519 AV-PGPVLIDIVDPNALSP 538
 DB 566 SYNDPRVVVDVIEDAMVWP 586

RESULT 15
 ID 09W218 PRELIMINARY: PRT: 584 AA.
 AC 09W218:
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE ACETOLACTATE SYNTHASE, LARGE SUBUNIT.
 GN TM0548.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogales; Thermotoga.
 OX NCBI_TaxId=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MSB8 / DSM 3109;
 RA MEDLINE=99287316; PubMed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 RT genome sequence of Thermotoga maritima.";
 RT Nature 399:323-329(1999).
 CC -1. SIMILARITY: WITH OTHER ENZYMES WHICH REQUIRE TPP.
 DB EMBL: AE001730; AAD35633.1;
 DR HSSP: P06169; 1PVD.
 DR TIGR: TM0548;
 DR INTERPRO: IPR000005;
 DR INTERPRO: IPR000399;
 DR PFAM: PF00205; TPP_enzymes; 1.
 DR PROSITE: PS00041; HTL_ARAQ_FAMILY_1; UNKNOWN_1.
 DR PROSITE: PS00187; TPP_ENZYMES; 1.
 KW Flavoprotein; Lyase; Thiamine pyrophosphate.
 SO SEQUENCE 584 AA; 64431 MW; B2F69C3D6A4F1205 CRC64;

Query Match 16.8%; Score 502.5; DB 2; Length 584;
 Best Local Similarity 27.1%; Pred. No. 3,4e-26;
 Matches 164; Conservative 103; Mismatches 232; Indels 107; Gaps 21;

QY 6 AEOLIDLEAGVKRYGLVGSLSNPIYDAV--ROSDIEVHNEEAFAAGAESLITG 63
 DB 9 SKMLFEALLKEGVDITFGIPGAIINVYDELCLNYEDKINFYLRHOGATTHAADGYART 68
 QY 64 ELAVCAASGPGNTILIGLVDLSHRNGAKVLAISHIPSAOISFPFOTHEPILKKEC 123
 DB 69 GRPGVYIVTSGPGATVYTGATATVMDSTPIYVITGOVPLSTIGTDAFQEDVDVTTGTP 128
 QY 124 GYCEVNGEGERILHNAIQ-----STMAGKSVSVVIIPGDIKAKEDAGDGTYSNST-I 177
 DB 129 TKHNHLVTSIEE---LPRAIKEMFYVATGGRGVPVLLDFPKDIOYAE-GEFNPVPTVEI 183

OY	178	SSGPRVPEPPTAEALAEALINNAKSVTLFCGAG--VNARAQVLEIAEKISPIGHALG	235
Db	184	PGYPTVYKGHPKQIKKAVELLEKSKRPVYLVGGANISGMDLVNPFIDKFVPAVSTLM	243
OY	236	GKQYIOHENPE-----VMSGLLCYGACVDASNEADLLILGTFPYSD-----	280
Db	244	GRGV-----NPEDEKLYEEGIGHQTY-YGVNVAAN--ADLITLIGVRF--SDRLIGNPT	294
OY	281	FLPNDNAQVINDINAHIGRRTYKYPTGTVNATIENTILPHVKEKIDRSFLDMLKAHR	340
Db	295	FAKNAARIVHVIDEAIEGKNVRDVPVIGDLKSVLEEF---KYELTFDSMWIEELQF-	350
OY	341	KLSSVETETYNHVKHP-----IHEVYASLIENTLADKDAVEYVDTCMGNWHAR	391
Db	351	-----IKKKPPLTKRDKGLIKRQYVEKVEVEFPDDTVVAQVGNQMWAAQ	398
OY	392	YIENEGTRDVGVSFRIGTANALPRAIGASQSDRNQVYIAMCGDDGLMLGELLTYKL	451
Db	399	FYKR-KHQRSTLCGGGLGTGTLAPAGIGAPDCEVVAFAGDGGFQNNIOELMTIKR	457
OY	452	HOLPLKAVFNNSLSIGWK-----LEMVLEGQPEFGTDHEEVNFAETIAAAGIK	500
Db	458	YNLPKTIIVMNKALIGWRQMOQLFENCRSATILSNPD-----FAKIAEAVGIK	508
OY	501	SVRLTDPKRVREQLAEALATAPGVLLDIYDP--NAL-STLPITITWEQVNGFSKATRIY	557
Db	509	AMRIETKPOVDEALEIKLAKSEKPLIHAVVDPAENVLPMVP-----	550
OY	558	FGGGVG 563	
Db	551	-GGDVG 555	

Search completed: March 17, 2001, 21:55:06
Job time: 2537 sec